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□1: AAC62840. R33083_1 [Homo sa...[gi:3702295]   BLink, Links
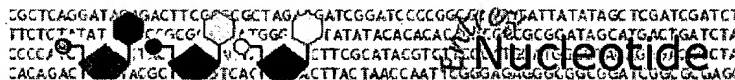
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LOCUS       AAC62840              432 aa            linear   PRI 05-OCT-1998
DEFINITION  R33083_1 [Homo sapiens].
ACCESSION   AAC62840
VERSION     AAC62840.1  GI:3702295
DBSOURCE    locus AC005783 accession AC005783.1
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 432)
  AUTHORS   Lamerdin,J.E., McCready,P.M., Skowronski,E., Viswanathan,V.,
            Burkhart-Schultz,K., Gordon,L., Dias,J., Ramirez,M., Stilwagen,S.,
            Phan,H., Velasco,N., Do,L., Regala,W., Terry,A., Garnes,J.,
            Danganan,L., Erler,A., Christensen,M., Georgescu,A., Avila,J.,
            Liu,S., Attix,C., Andreise,T., Trankheim,M., Amico-Keller,G.,
            Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G.,
            Kronmiller,B., Arellano,A., Saunders,C., Ow,D., Nolan,M., Trong,S.,
            Kobayashi,A., Olsen,A.S. and Carrano,A.V.
  TITLE     Sequence analysis of a 2.5 Mb region in 19p13.3
  JOURNAL   Unpublished
REFERENCE   2  (residues 1 to 432)
  AUTHORS   Lamerdin,J.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-OCT-1998) Joint Genome Institute, Lawrence Livermore
            National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
COMMENT     Method: conceptual translation supplied by author.
FEATURES             Location/Qualifiers
     source          1..432
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                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /map="19p13.3 between D19S883 and D19S325"
                     /clone="R33083"
                     /cell_line="5HL2-B"
                     /clone_lib="LL19NC03 R chromosome 19-specific cosmid
                     library"
                     /note="Cosmid library constructed at LLNL from flow-sorted
                     chromosomes from human-hamster hybrid 5HL2-B, which
                     carries chromosome 19 as its only human chromosome."
     Protein         1..>432
                     /product="R33083_1"
                     /name="Hypothetical partial human protein most similar to
                     Caenorhabditis elegans ORF encoded by (AF043699) contains
                     similarity to the"
     CDS             1..432
                     /coded_by="complement(join(AC005783.1:<263..342,
                     AC005783.1:2907..2968,AC005783.1:4718..4840,
                     AC005783.1:5294..5407,AC005783.1:6577..6745,
                     AC005783.1:6801..6995,AC005783.1:8549..8661,
                     AC005783.1:16772..17048,AC005783.1:17500..17661))"
                     /note="Should represent 5'-end of hypothetical protein
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☐ 1: AC005783. Homo sapiens chro...[gi:3702294]   Links

```
LOCUS       AC005783                43501 bp    DNA     linear   PRI 05-OCT-1998
DEFINITION  Homo sapiens chromosome 19, cosmid R33083, complete sequence.
ACCESSION   AC005783
VERSION     AC005783.1  GI:3702294
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 43501)
  AUTHORS   Lamerdin,J.E., McCready,P.M., Skowronski,E., Viswanathan,V.,
            Burkhart-Schultz,K., Gordon,L., Dias,J., Ramirez,M., Stilwagen,S.,
            Phan,H., Velasco,N., Do,L., Regala,W., Terry,A., Garnes,J.,
            Danganan,L., Erler,A., Christensen,M., Georgescu,A., Avila,J.,
            Liu,S., Attix,C., Andreise,T., Trankheim,M., Amico-Keller,G.,
            Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G.,
            Kronmiller,B., Arellano,A., Saunders,C., Ow,D., Nolan,M., Trong,S.,
            Kobayashi,A., Olsen,A.S. and Carrano,A.V.
  TITLE     Sequence analysis of a 2.5 Mb region in 19p13.3
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 43501)
  AUTHORS   Lamerdin,J.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-OCT-1998) Joint Genome Institute, Lawrence Livermore
            National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
COMMENT     Map and sequence oriented from p telomere to centromere. Cosmid
            R33083 overlaps R26894 (AC005594) to the left from bases 1 to 1,804
            of this accession, and overlaps cosmid R30140 to the right from
            bases 37,702 to 43,501. Additional chromosome 19 map and sequence
            information may be obtained at:
            http://www-bio.llnl.gov/bbrp/genome/genome.html.
FEATURES             Location/Qualifiers
     source          1..43501
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                     /db_xref="taxon:9606"
                     /chromosome="19"
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                     /clone="R33083"
                     /cell_line="5HL2-B"
                     /clone_lib="LL19NC03 R chromosome 19-specific cosmid
                     library"
                     /note="Cosmid library constructed at LLNL from flow-sorted
                     chromosomes from human-hamster hybrid 5HL2-B, which
                     carries chromosome 19 as its only human chromosome."
     misc_feature    complement(241..342)
                     /note="predicted exon, program: grail2exons_human_1.3,
                     frame: 1, quality: excellent, score: 87.000"
     CDS             complement(join(<263..342,2907..2968,4718..4840,
                     5294..5407,6577..6745,6801..6995,8549..8661,16772..17048,
                     17500..17661))
                     /note="Hypothetical partial human protein most similar to
                     Caenorhabditis elegans ORF encoded by (AF043699) contains
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                              similarity to the; Should represent 5'-end of hypothetical
                              protein R26894_1 encoded by AC005594. Predicted primarily
                              on basis of Xgrail and BLAST similarities"
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                              /evidence=not_experimental
                              /product="R33083_1"
                              /protein_id="AAC62840.1"
                              /db_xref="GI:3702295"
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                              EIPKKVRKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGITSYDFHSE
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                              AFFSFINNSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGY
                              WWCPTASWEEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRTGSKNPKIA
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repeat_region                 1161..1457
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repeat_region                 1568..1869
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                              /note="predicted exon, program: grail2exons_human_1.3,
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repeat_region                 3878..4178
                              /rpt_family="AluJo"
repeat_region                 complement(4200..4518)
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misc_feature                  complement(6577..6745)
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misc_feature                  complement(6801..6995)
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                              frame: 2, quality: excellent, score: 100.000"
misc_feature                  complement(7099..7216)
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repeat_region                 complement(7921..8174)
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                         frame: 2, quality: excellent, score: 100.000"
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        repeat_region    19047..19347
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        repeat_region    complement(19410..19515)
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        repeat_region    complement(20778..20911)
                         /rpt_family="FLAM_C"
        repeat_region    21752..22037
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        repeat_region    22038..22061
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        repeat_region    22167..22373
                         /rpt_family="MER20"
        misc_feature     22574..22678
                         /note="predicted exon, program: grail2exons_human_1.3,
                         frame: 2, quality: excellent, score: 82.000"
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                         /rpt_family="LINE2"
        repeat_region    23287..23494
                         /rpt_family="MER20"
        repeat_region    23740..23928
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        repeat_region    23946..24060
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        repeat_region    24191..24485
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                        variant gene for tRNA-Val (anticodon:CAC) and tRNA-Gly
                        (anticodon:UCC)"
     repeat_region      complement(26589..26625)
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                        /note="BLASTN similarity to X17515 (82..650); match: 0.99,
                        score: 2.4e-234; database searched: nt; Human gene for
                        variant cytoplasmic tRNA-Val(CAC)~BLASTN similarity to
                        X64281 (82..650); match: 1, score: 1.9e-234; database
                        searched: nt; H.sapiens variant gene for tRNA-Val
                        (anticodon:CAC) and tRNA-Gly (anticodon:UCC)"
     misc_feature       27206..27418
                        /note="BLASTN similarity to Z59776 (1..214); match: 0.98,
                        score: 1.9e-78; database searched: nt; H.sapiens CpG DNA,
                        clone 172e6, forward read cpg172e6.ft1a."
     misc_feature       complement(27206..27418)
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                        score: 1.0e-73; database searched: nt; H.sapiens CpG DNA,
                        clone 172e6, reverse read cpg172e6.rt1a."
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                        /note="BLASTN similarity to X64281 (69..84); match: 1,
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                        gene for tRNA-Val (anticodon:CAC) and tRNA-Gly
                        (anticodon:UCC)~BLASTN similarity to X17515 (69..84);
                        match: 1, score: 2.4e-234; database searched: nt; Human
                        gene for variant cytoplasmic tRNA-Val(CAC)"
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     repeat_region      29332..29630
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     repeat_region      29631..29705
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     repeat_region      30727..30758
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repeat_region          32531..33133
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repeat_region          34704..34999
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repeat_region          35003..35301
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repeat_region          36531..36588
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repeat_region          37470..37767
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repeat_region          37773..37852
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repeat_region          37963..38260
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repeat_region          complement(38939..39092)
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repeat_region          39199..39400
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repeat_region          39596..39728
                       /rpt_family="AluJo/FRAM"
repeat_region          39736..40037
                       /rpt_family="AluSx"
repeat_region          40039..40214
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repeat_region          40220..40345
                       /rpt_family="AluJo/FLAM"
repeat_region          40348..40644
                       /rpt_family="AluJo"
misc_feature           complement(41008..41050)
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         repeat_region   42558..42852
                         /rpt_family="AluSx"
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BASE COUNT     10740 a  11580 c  11888 g    9293 t
ORIGIN
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      121 ctgcgggaag acgtgagcag atggaaggaa tggcacggaa ggccaggagg cagcttcggt
      181 ggctgcccag ggcccagggc cctgcaggtg aattccttgg gttccagcca gagacactca
      241 ctatttgcca tcccgggtcc acccggccct ggcgatgtac tccaccttcg gaacagcga
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      361 gtgtgggtca tgccctggcc tgcccggcgc tgctcggagg agaaggccac tgcgctgggt
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      661 gagaaggagc cacctgctag cagcttggtg ttggacatta tcaatttcgg ccgtgtaagc
      721 ctcccagtct gtggtccttt gtcatggccc aaacaaatga ctacacccaa caggggcagg
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      901 ccatgcttaa acagggctgg cacggcgttt ccagggtatt gagagatagg ggacctgagc
      961 cttcctcgtg tctaaatggg gctggcacag catctctgga ggatcaaagg gagaaacggc
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     1201 gagaggctga ggcaggtgga tcacttgagg tcaggagttc gagaccagcc tggggaacat
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     1441 aaaacaagaa caaacaagca aagcaaaacc ccagcctgga aggaggtttc acgtgcatca
     1501 ctggcaaagc cactcagact gatcacctaa aatctgccag aatgctactg tcaagaatgc
     1561 aaaagaaggc cgggtgtggt ggctcacacc tgtaatccca cactttggg aggccgaggc
     1621 gggcggatca cgaggtcagg agattgagac cgtcctggct aacacggtga aaccccgtct
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     2101 gacacccttc tgggtcttat gggatttgca acttccgaga gaactgatca atgtggggct
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     2221 ggggtggcta cggaggaggg ggccgaggga gatgcggtca caggtgtggt ctgctggtga
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     2461 gaggatctgc ctgaaacgct ggaggaaaca gcccgtccga agttggggtc ccccagccat
     2521 ctgccccacg gagttctctg ttctggaaac ttggagagag ggcagctctg gatccacacg
     2581 tcacccactc ccgaggtggc ctgggagcac ctgccgcgcc tgtcctcgca gggcccctgc
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43501 c
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